

1 MEA--EQAAGASEGATPGLAVPEVAPBPAT-----hHac3.pro  
1 -----hHac2.pro  
1 MDRGGGRGESPGATPAEGPPPPPEAPPEGPGAPPQHPPRAEALPPEAADEGGPRGRhHac1.pro  
32 -----AASGP-----hHac3.pro  
1 -----hHac2.pro  
61 LRSRDSSCGRPGTPGAATAKSPNGECGRGEPQCSPAGPEGPARGPKVSFSCRGAASGP-----hHac1.pro  
37 IEKSGP-----EBK-----RRHLGLLLOPTVKNKFSLRVFGSHKAVEIEQEhHac3.pro  
1 -----KEQE-----hHac2.pro  
121 AEGPGEAAEAGSEAGPACEPGRGSQASFMQRFQFALLQBGVNKFSLRMFGSQKAVEIEQEhHac1.pro  
77 RVKSAGAWIIHPYSDFRYWDLIMLIMVGNLIIVLPVGITFFKEENSPPWIVFNVLSDTFhHac3.pro  
5 RVKTAGFWIIHPYSDFRYWDLIMLIMVGNLIIVIPVGITFFIEQITTPWLIIFNVASDTVhHac2.pro  
181 RVKSAGAWIIHPYSDFRYWDFTMLLIFMVGNLIIPVGITFFKDETAPWIVFNVLSDTFhHac1.pro  
137 FLDDLVLNFRGTGIVVEGAELIAERARTRYLRTWELVDLISSIPVDYIFLIVLEPRLhHac3.pro  
65 FLDDLIMNFRGTGIMNEDSEIILDEKVIKMNLYLKSFWVDFFISSIPVDYIFLIVEKG--MhHac2.pro  
241 FLDDLVLNFRGTGIVIEDNTEIILDEBEKIKKYLRTWFWVDVMSSIPVDYIFLIVEKG--IhHac1.pro  
197 DAEVYKTARALRIVRFTKILSLLRLLRSLRLIRYIHQWEEIFHMTYDLASAVVRIFNLIghHac3.pro  
123 DSEVYKTARALRIVRFTKILSLLRLLRSLRLIRYIHQWEEIFHMTYDLASAVVRIFNLIghHac2.pro  
299 DSEVYKTARALRIVRFTKILSLLRLLRSLRLIRYIHQWEEIFHMTYDLASAVVRIFNLIghHac1.pro  
257 MMLLLCHWDFCLQFLVPMLQDFPPDCWVSINIMVNHSWGRQYSHALFKAMSHMLCIGYQhHac3.pro  
183 MMLLLCHWDFCLQFLVPLQDFPPDCWVSINIMVNNDSWGKQYSYALFKAMSHMLCIGYGAhHac2.pro  
359 MMLLLCHWDFCLQFLVPMLQDFPNCWVSINIMVNHSWSELYSFALFKAMSHMLCIGYGRhHac1.pro  
317 QAPVGMFDVWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac3.pro  
243 QAPVMSDILWLTMLSMIVGATCYAMFVGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac2.pro  
419 QAPFSMTDILWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRRQYQEKYQVEQYMSFHKLhHac1.pro

FIG. 1A.

377 PADTRQRIHEIYEYEHRYQGKMFDEESILGELSEPLREEIINFTCRGLVAHMPLEFAHADPSF hHac3.pro  
303 PADMRQKIHDYEHRYQGKIIFDEENIINELNDPLREEIVNFCRKLVAITMPLFANADPNF hHac2.pro  
479 PADFRQKIHDYEHRYQGKMFDEDSILGELNGPLREEIVNFCRKLVASMPLEFANADPNF hHac1.pro

437 VTAMLTKLRFEFVQPGDLVVREGSVGRKMYFIZHGLLSVLARGARDTRLTGSGYFGEICL hHac3.pro  
363 VTAMLKSLRFEFVQPGDYIIREGAVGKKMYFIZHGVAGVITKSSKEMKLTGSGYFGEICL hHac2.pro  
539 VTAMLTKLRFEFVQPGDYIIREGTIGKKMYFIZHGVSVLTGKNGKEMKLSGSGYFGEICL hHac1.pro

497 LTRGRRRTASVRADTYCRLYSLSDVDFNAVLEEFPMRRRAFETVAMDRLIRIGKKNSILQR hHac3.pro  
423 LTRGRRRTASVRADTYCRLYSLSDVDFNEVLEEYPMRRRAFETVAIDRLDRIGKKNSILIQ hHac2.pro  
599 LTRGRRRTASVRADTYCRLYSLSDVDFNEVLEEYPMRRRAFETVAIDRLDRIGKKNSILIH hHac1.pro

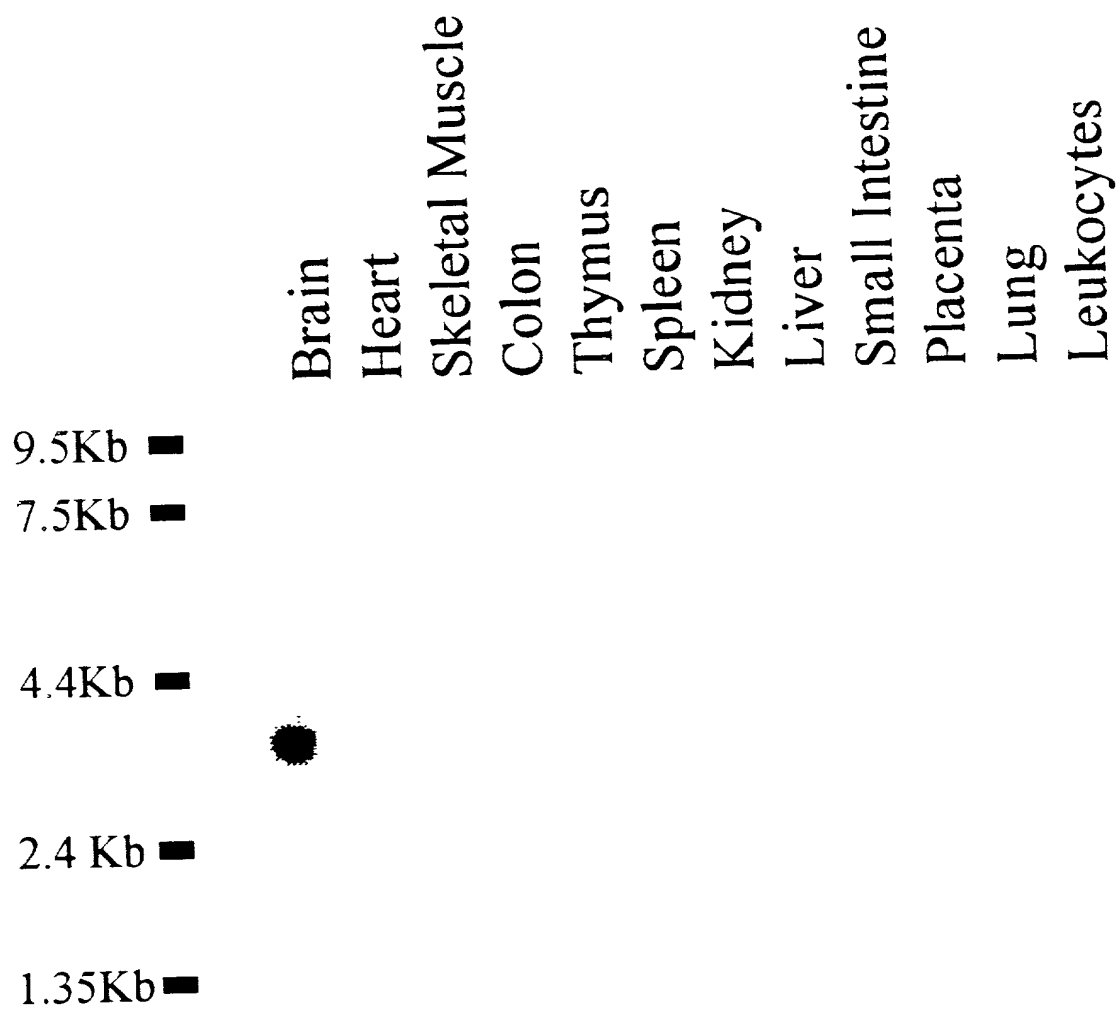
557 R-RSEPSPG--SSGGIMEHLVQHDRDMARGVGRAPSTGAQLSGKPVLWEPLVHAPLQ hHac3.pro  
483 KFKQKDLNTGVFNQENELKQIVKHDREMVQAIAPINYPQMTILNSTSTTTETSRMRTQ hHac2.pro  
459 KVQHDNLNSGVFNQENALITQELVKVDREMVQQA---ELGQRVGL----- hHac1.pro

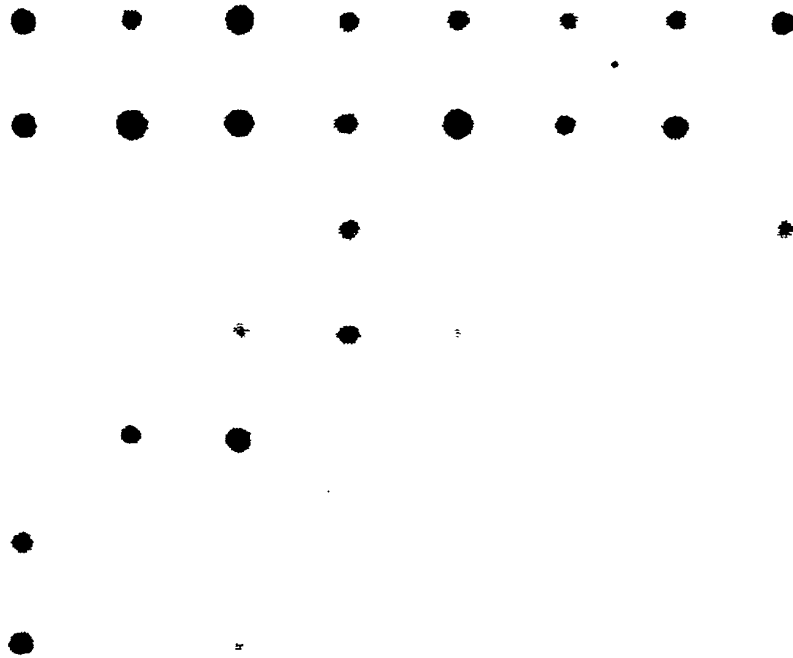
613 AAATTSNVAIALTHQRGPIPLSP-DSPATLTARSAMRSAGSPA--SPLVPVR--AGPW hHac3.pro  
543 SPVVTATSLSHSNLHSPSTQTQPSAILSPCSYTTAVCSPPMOQSPIAARTFHYASPT hHac2.pro  
700 -----FPPPPPPPPQVTSATATLQQA-AMSFCEQVARELVGP-LALGSPR hHac1.pro

666 ASTSRLEAF-PARTLHASLSRAAGRSQVSLGPPPGGG-----GRRIGPR hHac3.pro  
603 ASQLSLMQQQPQQVQSQPQRQQQF-SPPQPTPGSSTPKNEVHKSTQAIHNTNLTRE hHac2.pro  
743 LVRRPPGGAFAAASPGPPPASPPGAFASPRAPRTSPYGGLPAAAPLAGPALPARRLSRA hHac1.pro

709 GRPLSASQPSLPQRAITCDGSPGRKSGS-ERI-----PPSGILAKPPRTAQPP-- hHac3.pro  
662 VRPEASMQPSLPHEVS--TLISRPHTVCELSIASIPQPVTAVPGTGLQAGGRSTVPQRV hHac2.pro  
803 SRPLSASQPSLPHGAPCPAASPTRFASSTPRLGPTPAARAAPSPDRRDSASPGAAGGL- hHac1.pro

756 --RPPVPPEATPRGLQLSANM. hHac3.pro  
720 FFRQMSSGAIPENRGVLPAPPLITPHPKK hHac2.pro  
862 -----DEQDSARSLSSNL. hHac1.pro

*FIG. 2A.*



whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
appendix	lung	trachea	placenta				
fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	

FIG. 2B.

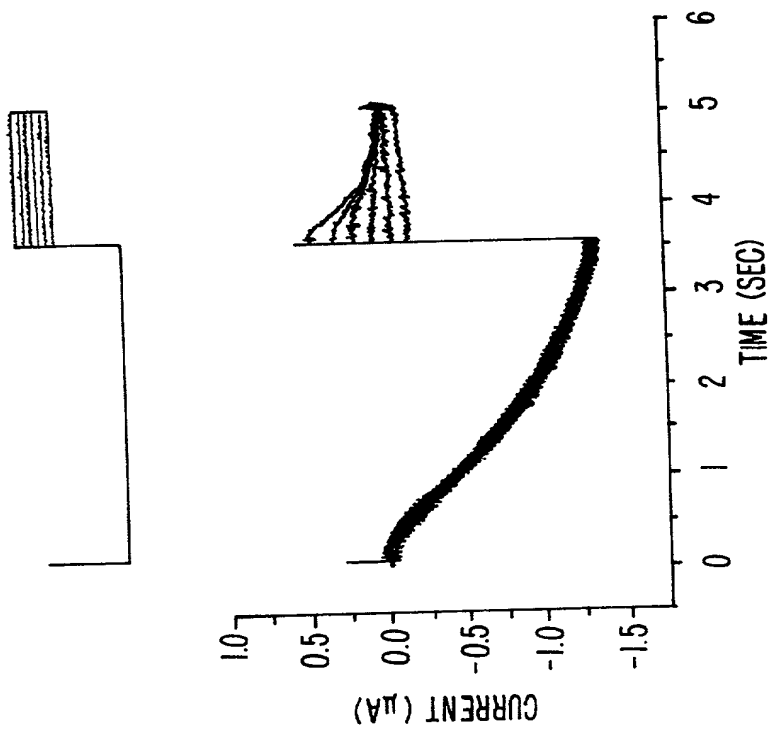


FIG. 3B.

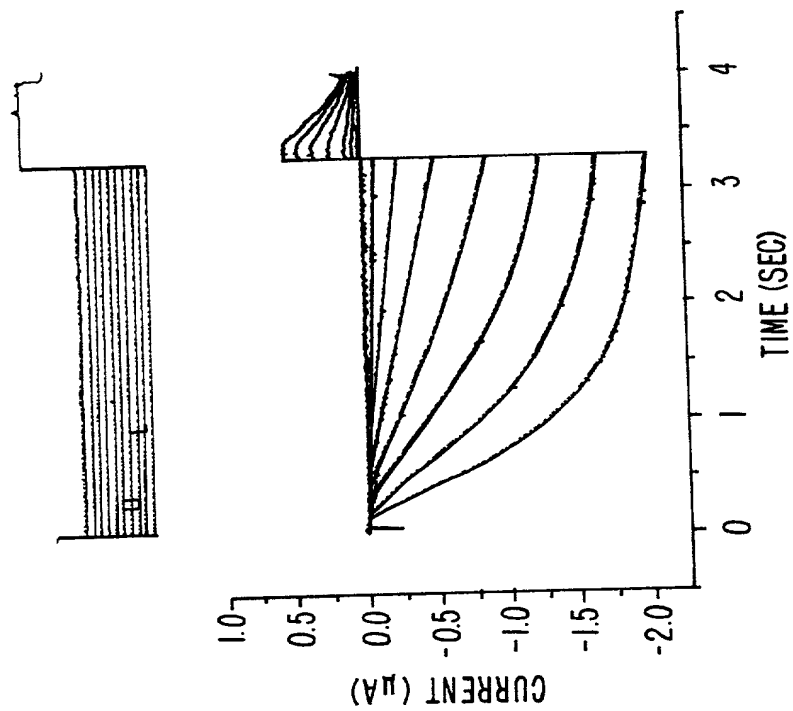


FIG. 3A.

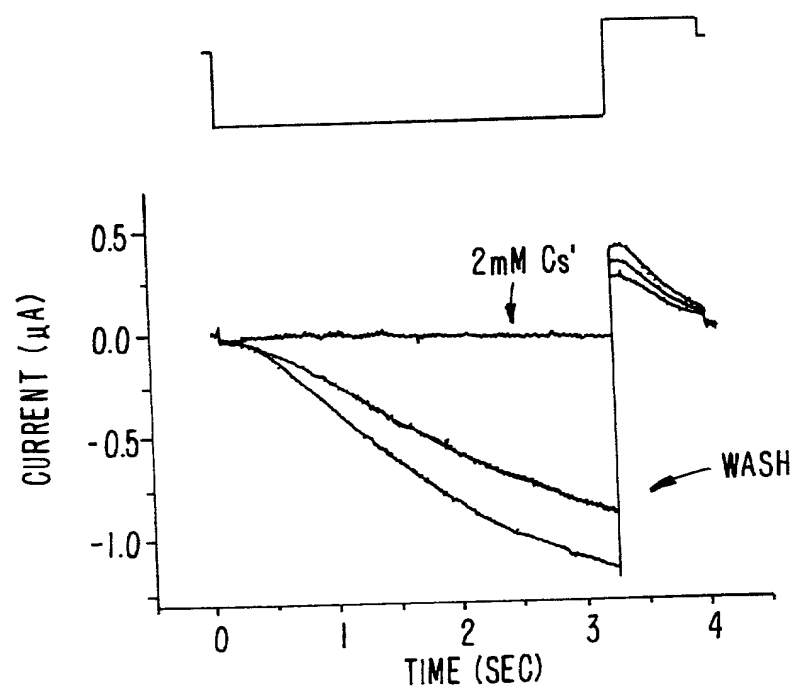


FIG. 4.